

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: IPK Gatersleben
- (B) STREET: Corrensstr. 3
- (C) CITY: Gatersleben
- (E) COUNTRY: Germany
- (F) ZIP CODE: 06466

(ii) TITLE OF INVENTION: 2-Deoxyglucose-6-phosphate (2-DOG-6-P)
phosphatase DNA sequences as selection marker in plants

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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(iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/FEATURE: CDS

(B) LOCATION: 9..746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGATCCCC ATG GCA GAA TTT TCA GCT GAT CTA TGT CTT TTT GAC CTA GAT	50
Met Ala Glu Phe Ser Ala Asp Leu Cys Leu Phe Asp Leu Asp	
1 5 10	
 GGT ACC ATA GTG AGT ACA ACA GTG GCC GCA GAG AAA GCA TGG ACC AAG	98
Gly Thr Ile Val Ser Thr Thr Val Ala Ala Glu Lys Ala Trp Thr Lys	
15 20 25 30	
TTG TGT TAC GAA TAC GGT GTT GAT CCT TCC GAG TTA TTT AAG CAT TCT	146
Leu Cys Tyr Glu Tyr Gly Val Asp Pro Ser Glu Leu Phe Lys His Ser	
35 40 45	
 CAT GGT GCA AGA ACA CAA GAG GTT TTG AGA AGG TTT TTC CCT AAA TTG	194
His Gly Ala Arg Thr Gln Glu Val Leu Arg Arg Phe Phe Pro Lys Leu	
50 55 60	
 GAT GAT ACA GAC AAT AAA GGT GTT CTT GCT CTA GAA AAA GAT ATT GCC	242
Asp Asp Thr Asp Asn Lys Gly Val Leu Ala Leu Glu Lys Asp Ile Ala	
65 70 75	
 CAT AGT TAC TTG GAT ACA GTA AGC CTT ATT CCT GGT GCA GAG AAC TTA	290
His Ser Tyr Leu Asp Thr Val Ser Leu Ile Pro Gly Ala Glu Asn Leu	
80 85 90	
 CTG TTA TCG TTA GAT GTA GAT ACT GAG ACT CAA AAA AAG TTA CCT GAA	338
Leu Leu Ser Leu Asp Val Asp Thr Glu Thr Gln Lys Lys Leu Pro Glu	
95 100 105 110	

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AGG AAA TGG GCT ATC GTT ACC TCT GGT TCT CCA TAT TTG GCA TTT TCA 386
 Arg Lys Trp Ala Ile Val Thr Ser Gly Ser Pro Tyr Leu Ala Phe Ser
 115 120 125

TGG TTC GAG ACA ATA TTG AAA AAT GTT GGA AAG CCC AAA GTT TTC ATT 434
 Trp Phe Glu Thr Ile Leu Lys Asn Val Gly Lys Pro Lys Val Phe Ile
 130 135 140

ACT GGG TTT GAC GTG AAG AAC GGT AAG CCT GAT CCC GAG GGT TAT TCA 482
 Thr Gly Phe Asp Val Lys Asn Gly Lys Pro Asp Pro Glu Gly Tyr Ser
 145 150 155

AGA GCT CGT GAT TTA TTG CGT CAA GAT TTG CAA TTA ACT GGT AAA CAG 530
 Arg Ala Arg Asp Leu Leu Arg Gln Asp Leu Gln Leu Thr Gly Lys Gln
 160 165 170

GAT CTG AAG TAT GTT GTC TTC GAA GAT GCA CCC GTG GGC ATA AAG GCC 578
 Asp Leu Lys Tyr Val Val Phe Glu Asp Ala Pro Val Gly Ile Lys Ala
 175 180 185 190

GGC AAA GCA ATG GGC GCC ATT ACT GTG GGT ATA ACA TCC TCG TAT GAC 626
 Gly Lys Ala Met Gly Ala Ile Thr Val Gly Ile Thr Ser Ser Tyr Asp
 195 200 205

AAG AGC GTT TTA TTT GAC GCA GGA GCA GAT TAT GTA GTC TGT GAT TTG 674
 Lys Ser Val Leu Phe Asp Ala Gly Ala Asp Tyr Val Val Cys Asp Leu
 210 215 220

ACA CAG GTT TCC GTG GTT AAG AAC AAT GAA AAC GGT ATT GTC ATC CAG 722
 Thr Gln Val Ser Val Val Lys Asn Asn Glu Asn Gly Ile Val Ile Gln
 225 230 235

GTA AAC AAC CCT TTG ACA AGG GCC TGAGTAGTCG AC 758
 Val Asn Asn Pro Leu Thr Arg Ala
 240 245

005670 422500

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Glu Phe Ser Ala Asp Leu Cys Leu Phe Asp Leu Asp Gly Thr
 1 5 10 15
 Ile Val Ser Thr Thr Val Ala Ala Glu Lys Ala Trp Thr Lys Leu Cys
 20 25 30
 Tyr Glu Tyr Gly Val Asp Pro Ser Glu Leu Phe Lys His Ser His Gly
 35 40 45
 Ala Arg Thr Gln Glu Val Leu Arg Arg Phe Phe Pro Lys Leu Asp Asp
 50 55 60
 Thr Asp Asn Lys Gly Val Leu Ala Leu Glu Lys Asp Ile Ala His Ser
 65 70 75 80
 Tyr Leu Asp Thr Val Ser Leu Ile Pro Gly Ala Glu Asn Leu Leu Leu
 85 90 95
 Ser Leu Asp Val Asp Thr Glu Thr Gln Lys Lys Leu Pro Glu Arg Lys
 100 105 110
 Trp Ala Ile Val Thr Ser Gly Ser Pro Tyr Leu Ala Phe Ser Trp Phe
 115 120 125
 Glu Thr Ile Leu Lys Asn Val Gly Lys Pro Lys Val Phe Ile Thr Gly
 130 135 140
 Phe Asp Val Lys Asn Gly Lys Pro Asp Pro Glu Gly Tyr Ser Arg Ala
 145 150 155 160

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Arg Asp Leu Leu Arg Gln Asp Leu Gln Leu Thr Gly Lys Gln Asp Leu
 165 170 175

Lys Tyr Val Val Phe Glu Asp Ala Pro Val Gly Ile Lys Ala Gly Lys
 180 185 190

Ala Met Gly Ala Ile Thr Val Gly Ile Thr Ser Ser Tyr Asp Lys Ser
 195 200 205

Val Leu Phe Asp Ala Gly Ala Asp Tyr Val Val Cys Asp Leu Thr Gln
 210 215 220

Val Ser Val Val Lys Asn Asn Glu Asn Gly Ile Val Ile Gln Val Asn
 225 230 235 240

Asn Pro Leu Thr Arg Ala
 245

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: YES

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGGATCCCC ATGGCAGAAT TTTCAGCTGA TCTATG

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: YES

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGTCGACTA CTCAGGCCCT TGTCAAAGGG TTG

33

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